

## The Crystal Structure of Methyl $\beta$ -Maltopyranoside

By SHIRLEY S. C. CHU AND G. A. JEFFREY

*The Crystallography Laboratory, The University of Pittsburgh, Pittsburgh, Pa. 15213, U.S.A.*

(Received 11 January 1967)

The crystal structure of methyl  $\beta$ -maltoside monohydrate was solved by the convolution of the Patterson projection with  $E$  maps obtained by a sign-correlation procedure on the  $h0l$  reflections. The structure was refined three-dimensionally by anisotropic least squares to give a final  $R$  value of 0.056 for 1375 reflections. The space group is  $C2$ , with  $Z=4$  and unit-cell dimensions  $a=22.664$ ,  $b=4.841$ ,  $c=17.316$  Å,  $\beta=117.27^\circ$ . All the hydrogen atoms were located on difference syntheses, but were not refined. The  $\alpha$  1-4 linked glucopyranose residues have the  $C1$  chair conformation with interatomic distances which are normal for single bonds, with the exception of the C-O bonds. The methyl  $\beta$ -glycosidic bond, C(1')-O(1')CH<sub>3</sub>, is 1.375 Å. It is significantly shorter than the mean value of 1.427 Å, in contrast to the  $\alpha$ -glycosidic link joining the two glucopyranoside residues, which is 1.416 Å. This difference in the glucosidic bond lengths appears to be correlated with the relative lengths of the C-O ring bonds, which are observed equal in one ring (C'-O') and unequal in the other (C-O). All the oxygen atoms, except the ring and bridge oxygen atoms, are associated with a hydrogen bonding scheme, which includes one intramolecular bond and consists of closed rings and helical chains.

### Introduction

Maltose is an important disaccharide, of considerable interest as a model compound for the structure of amylose and starch. Hybl, Rundle & Williams (1965) have determined the crystal structure of the cyclohexaamylose-potassium acetate complex which contains the equivalent of three maltose units. It is the purpose of this investigation to determine the detailed conformation of the maltose molecule and provide more precise data on interatomic distances and the hydrogen bonding in the solid state.

Maltose was shown by Haworth, Long & Plant (1927) to consist of two D-glucopyranose residues connected between carbon atoms 1 and 4 by an  $\alpha$ -glucosidic link, thereby differing from cellobiose, which has a similar structure with a  $\beta$  1-4 linkage. Bentley (1959) concluded from chemical evidence that in cellobiose both glucose units have the chair-shaped  $C1$  conformation and this has been confirmed by the crystal structure determination (Jacobson, Wunderlich & Lipscomb, 1961; Brown, 1966). Bentley's results on maltose were less definitive, since he assumed that both glycosidic bonds were equatorial and interpreted the observed complexing reactions with cuprammonium solution to require a 'skew' intermediate for the non-reducing glucose unit. We have examined the methyl glucoside derivative rather than maltose itself because these results referred more directly to that compound.

### Crystal data

Methyl  $\beta$ -maltoside monohydrate crystals were obtained through the courtesy of Dr Bentley (Bentley, 1959) of the Graduate School of Public Health, University of Pittsburgh. They were in the form of thin, transparent needles elongated along the  $b$  axis. The cell par-

ameters were measured with Cu  $K\alpha_1$  and Cu  $K\alpha_2$  radiation on a Picker 4-angle automatic diffractometer. The crystal density was determined by flotation in a liquid mixture of carbon tetrachloride and carbon disulfide.

Methyl  $\beta$ -maltoside monohydrate, C<sub>13</sub>O<sub>11</sub>H<sub>24</sub>.H<sub>2</sub>O, M.W. 374.35.

Monoclinic, space group  $C2$  from the systematic extinctions:  $hkl$  absent for  $h+k=2n+1$ .

$a=22.644$  ( $\sigma=0.009$ ) Å

$b=4.841$  ( $\sigma=0.003$ )

$c=17.316$  ( $\sigma=0.007$ )

$\beta=117.27$  ( $\sigma=0.05$ )°

$Z=4$

$D_m=1.469$  ( $\sigma=0.004$ ) g.cm<sup>-3</sup>

$D_x=1.472$  g.cm<sup>-3</sup>

$\mu_{Cu K\alpha}=11.54$  cm<sup>-1</sup>.

### Experimental

The integrated intensity data were recorded initially on multiple-film equi-inclination Weissenberg photographs with Cu  $K\alpha$  radiation. Of the 2169 theoretically possible reflections, 1256 were observed above the background of the film, and their intensities were estimated visually by comparison with a standard scale. No absorption corrections were made. The intensities were correlated and reduced to the structure amplitudes using an IBM 7090 program (Shiono, 1966a) which was based on the procedure by Hamilton, Rollett & Sparks (1965).

After the structure was solved, another set of data was collected on a Picker 4-angle automatic diffractometer from a crystal with approximate dimensions of 0.02 × 1.00 × 0.15 mm. A  $\theta/2\theta$  scanning mode over 2° was used to measure 1602 independent reflections with  $2\theta$  values below 130°, of which 1375 reflections had

intensities significantly above the background. Stationary background measurements were made at both ends of the  $2^\circ$  scan range of each reflection. The same number of equivalent reflections were measured in two different quadrants of the reciprocal lattice. However, the reference reflections which were repeated in intervals of approximately every 100 reflections were found to be significantly more constant for one set and these data were used in the refinement rather than the mean values. No absorption corrections were applied in reducing to structure amplitudes.

### Determination of the structure

The structure was solved from the 307 observed  $h0l$  reflections. The structure factors were converted to the normalized  $|E_{hkl}|$ 's (Hauptman & Karle, 1953), two linearly independent reflections were arbitrarily given positive signs in order to fix the origin and twelve more reflections with large  $|E|$  values were given symbolic signs. The Beurskens (1963) IBM 1620 program was then used to determine the most probable values of the symbols by first applying the Sayre (1952) equation to obtain sign relationships and then eliminating unknowns by a sign correlation procedure. Since the centrosymmetric projection of a monoclinic space group lacks the symmetry relations which generate negative signs, the trivial set of all positive signs has the highest probability. The four symbols of lowest probability were therefore given all combinations of plus and minus signs, except all positive, leaving 15 possible solutions of 90 to 120 signs each. Of the fifteen alternative two-dimensional  $E$  maps (Karle, Hauptman, Karle & Wing, 1958) five showed some features of the molecule, but it was impossible to select the correct one. A two-dimensional ( $E^2 - 1$ ) Patterson synthesis indicated the orientation of the pyranose rings but could not be interpreted in detail. Each of the five most probable trial  $E$  maps was therefore convoluted with the Patterson function by finite integration, using an IBM 1620 program prepared by Corfield (1965). This led to a recognition of the structure in one of the possible solutions. The first structure factor calculation for thirteen carbons and twelve oxygens gave an  $R$  value of 0.52 for all observed reflections. Successive Fourier syntheses, difference Fourier syntheses, and some trial and error calculations led to an isotropic least-squares refinement which gave an  $R$  value of 0.18 for the  $h0l$  data. By fixing one particular atom, the  $y$  coordinates were then easily determined using an assumed configuration of the molecule consistent with the resolved projection. Two cycles of isotropic least-squares refinement with the three-dimensional data gave an  $R$  value of 0.19.

### Refinement of the structure

The refinement of the positional parameters, the anisotropic thermal parameters for the carbon and oxygen

atoms, and one scale factor was carried out by the full-matrix least-squares IBM 7090 program on the intensity data collected by Picker diffractometer. The full-matrix least-squares program used was written by Busing, Martin & Levy (1962) for an IBM 7090 computer and modified by Shiono (1966*b*). Hughes's (1941) weighting scheme was used initially but Cruickshank's (1961) weighting scheme was substituted in the final stage in order to make  $[\sum w(F_{\text{obs}} - F_{\text{cal}})^2 / (\text{no. of reflections} - \text{no. of parameters})]^{1/2}$  approximately equal to unity. Because of the limited number of parameters that could be simultaneously varied by the program, each cycle of refinement was carried out in two stages by fixing the thermal parameters of eight neighboring atoms in each stage. Two cycles of anisotropic least-squares refinement reduced  $R$  to 0.077. All the hydrogen atoms except one on the methyl group, which is located near the direction of the large thermal motion of the carbon atom, were clearly revealed in two successive difference Fourier syntheses, with reasonable bond lengths and bond angles with respect to the carbon and oxygen atoms. Two more cycles of least-squares refinement, including all the hydrogen atoms, gave the final  $R$  value of 0.056. The positional parameters of the hydrogen atoms were not refined and they were assigned the same thermal parameters as those of the carbon or oxygen atoms to which they are bonded. The final positional and thermal parameters are listed in Table 1, and the corresponding structure factors are given in Table 2. The principal axes of the thermal ellipsoids are given in Table 3.

### Description of the structure

The systematic name for methyl  $\beta$ -maltoside monohydrate is methyl 4-*O*- $\alpha$ -D-glucopyranosyl- $\beta$ -D-glucopyranoside monohydrate (or methyl *O*- $\alpha$ -D-glucopyranosyl-(1 $\rightarrow$ 4)- $\beta$ -D-glucopyranoside monohydrate). The identification of the atoms used in this paper is shown in Fig. 1.

Both pyranose rings have the chair  $C_1$  form and there is no evidence of any departure from this strainless conformation towards a skew form such as suggested by Bentley (1959). The conformation angles of the rings are given in Table 4. They are in the same range as those observed in other pyranose sugars (*cf.* Kim & Jeffrey, 1967). The conformation about the  $\alpha$  1-4 linkage is such that the midplanes O(1')C(1')C(4'), O(4)C(4)O(1) through the glucose units make angles of  $171^\circ$  and  $165^\circ$  respectively with the plane of the C(4')O(1)C(1) link. This small twist in the 'backbone' of the molecule is such as to bring the intramolecular hydrogen-bonded O(2) and O(3') closer and leave more space between the primary alcohol groups for the hydrogen-bonded water on the other side of the molecule. It is worth remarking that the maltose 'backbone' in this structure is straighter than that observed in cellobiose (Brown, 1966), where the comparable angles are  $165^\circ$  and  $138^\circ$ , again with the twist so as to shorten the

intramolecular hydrogen-bond distance on one side of the molecule. The conformation angles of the primary alcohol groups are such that C(6)–O(6) has the '+sc' (+syn-clinal) (Klyne & Prelog, 1960) orientation, as was found in all the glucose residues in both cyclohexaamylose–potassium iodide (Hybl *et al.*, 1965) and cellobiose (Brown, 1966). The C(6')–O(6') bond has the

'–sc' (–syn-clinal) orientation, as was found in sucrose (Brown & Levy, 1963).

Within one molecular unit of methyl  $\beta$ -maltoside monohydrate, there are three hydrogen bonds. One is formed between O(2) and O(3') on one side of the molecule, and the other two link the water molecule with the two primary alcohol groups, O(6)H and

Table 1. *Fractional atomic coordinates and thermal parameters\**

The estimated standard deviations are given in parentheses and refer to the last decimal positions of respective values. The expression for the temperature factor exponent consistent with the  $\beta$  values is:

$$-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl).$$

	<i>x</i>	<i>y</i>	<i>z</i>	$\beta_{11}$	$\beta_{22}$	$\beta_{33}$	$\beta_{12}$	$\beta_{13}$	$\beta_{23}$
O(1)	0.3740 (2)	0.0000	0.1920 (2)	0.0016 (1)	0.0235 (16)	0.0027 (1)	–0.0009 (3)	0.0012 (1)	–0.0012 (4)
O(2)	0.3363 (2)	0.2878 (13)	0.0376 (2)	0.0016 (1)	0.0393 (21)	0.0028 (1)	0.0020 (4)	0.0008 (1)	0.0036 (5)
O(3)	0.4224 (2)	–0.0017 (14)	–0.0160 (2)	0.0021 (1)	0.0551 (26)	0.0023 (1)	0.0042 (5)	0.0010 (1)	0.0013 (6)
O(4)	0.5314 (2)	–0.2924 (12)	0.1146 (2)	0.0018 (1)	0.0353 (22)	0.0034 (2)	0.0021 (4)	0.0014 (1)	0.0010 (5)
O(5)	0.4825 (2)	0.1633 (12)	0.2452 (2)	0.0013 (1)	0.0277 (16)	0.0026 (1)	–0.0009 (3)	0.0007 (1)	–0.0023 (4)
O(6)	0.5893 (2)	–0.1118 (12)	0.3797 (2)	0.0020 (1)	0.0340 (20)	0.0025 (1)	–0.0001 (4)	0.0007 (1)	0.0010 (5)
C(1)	0.4152 (2)	0.2130 (14)	0.1877 (3)	0.0015 (1)	0.0214 (22)	0.0031 (2)	0.0000 (4)	0.0011 (1)	0.0004 (6)
C(2)	0.4044 (2)	0.2303 (14)	0.0948 (3)	0.0017 (1)	0.0240 (24)	0.0028 (2)	0.0008 (4)	0.0011 (1)	–0.0003 (6)
C(3)	0.4287 (2)	–0.0292 (14)	0.0693 (3)	0.0019 (1)	0.0213 (22)	0.0028 (2)	0.0004 (4)	0.0013 (1)	–0.0006 (6)
C(4)	0.5024 (2)	–0.0550 (14)	0.1336 (3)	0.0017 (1)	0.0247 (24)	0.0030 (2)	–0.0004 (4)	0.0010 (1)	0.0001 (6)
C(5)	0.5099 (2)	–0.0801 (15)	0.2259 (3)	0.0014 (1)	0.0298 (23)	0.0030 (2)	–0.0004 (5)	0.0010 (1)	0.0016 (6)
C(6)	0.5827 (2)	–0.0927 (17)	0.2938 (3)	0.0014 (1)	0.0430 (29)	0.0031 (2)	0.0006 (6)	0.0008 (1)	0.0018 (8)
O(1')	0.2065 (2)	–0.0591 (15)	0.3382 (2)	0.0020 (1)	0.0653 (31)	0.0037 (2)	–0.0013 (5)	0.0017 (1)	–0.0021 (7)
O(2')	0.1538 (2)	–0.1223 (14)	0.1537 (2)	0.0013 (1)	0.0569 (28)	0.0032 (2)	–0.0018 (4)	0.0006 (1)	–0.0025 (6)
O(3')	0.2403 (2)	0.1351 (13)	0.0910 (2)	0.0016 (1)	0.0453 (24)	0.0022 (1)	–0.0013 (4)	0.0003 (1)	0.0008 (5)
O(5')	0.3095 (2)	–0.0063 (12)	0.3511 (2)	0.0015 (1)	0.0395 (20)	0.0023 (1)	–0.0005 (4)	0.0008 (1)	–0.0005 (5)
O(6')	0.4302 (2)	0.3018 (12)	0.3949 (2)	0.0017 (1)	0.0307 (19)	0.0032 (2)	0.0000 (4)	0.0005 (1)	–0.0004 (5)
C(1')	0.2455 (2)	–0.1211 (16)	0.2986 (3)	0.0015 (1)	0.0366 (26)	0.0028 (2)	–0.0011 (5)	0.0011 (1)	–0.0018 (7)
C(2')	0.2148 (2)	0.0079 (15)	0.2092 (3)	0.0013 (1)	0.0345 (25)	0.0031 (2)	–0.0001 (5)	0.0008 (1)	–0.0014 (7)
C(3')	0.2617 (2)	–0.0275 (15)	0.1681 (3)	0.0011 (1)	0.0357 (25)	0.0022 (2)	–0.0012 (5)	0.0005 (1)	0.0001 (6)
C(4')	0.3313 (3)	0.0653 (14)	0.2304 (3)	0.0012 (1)	0.0303 (24)	0.0026 (2)	–0.0003 (4)	0.0009 (1)	–0.0013 (6)
C(5')	0.3550 (2)	–0.0730 (15)	0.3179 (3)	0.0014 (1)	0.0273 (23)	0.0030 (2)	0.0012 (5)	0.0011 (1)	0.0001 (6)
C(6')	0.4241 (3)	0.0067 (16)	0.3852 (3)	0.0020 (1)	0.0356 (28)	0.0022 (2)	0.0010 (6)	0.0009 (1)	0.0005 (7)
C(7')	0.2257 (3)	–0.2038 (27)	0.4178 (4)	0.0029 (2)	0.1091 (74)	0.0034 (3)	–0.0040 (11)	0.0018 (2)	–0.0002 (13)
O(W)	0.5643 (2)	0.3990 (14)	0.4424 (2)	0.0023 (1)	0.0454 (25)	0.0030 (2)	–0.0020 (5)	0.0009 (1)	0.0003 (6)

	<i>x</i>	<i>y</i>	<i>z</i>
H(O2)†	0.311	0.135	0.064
H(O3)	0.387	0.125	–0.060
H(O4)	0.542	–0.275	0.071
H(O6)	0.568	0.055	0.379
H(C1)	0.409	0.375	0.220
H(C2)	0.428	0.415	0.092
H(C3)	0.405	–0.205	0.076
H(C4)	0.526	0.120	0.129
H(C5)	0.485	–0.250	0.227
H(C6–1)	0.602	0.100	0.292
H(C6–2)	0.609	–0.250	0.290
H(O2')	0.109	–0.085	0.157
H(O3')	0.218	0.055	0.042
H(O6')	0.501	0.380	0.412
H(C1')	0.250	–0.330	0.292
H(C2')	0.210	0.235	0.210
H(3')	0.253	–0.250	0.154
H(C4')	0.331	0.290	0.231
H(C5')	0.354	–0.300	0.310
H(C6'–1)	0.460	–0.050	0.365
H(C6'–2)	0.428	–0.100	0.442
H(C7'–1)	0.270	–0.140	0.463
H(C7'–2)	0.192	–0.180	0.443
H(C7'–3)‡	0.225	–0.420	0.405
H(OW–1)	0.586	0.520	0.425
H(OW–2)	0.586	0.455	0.505

† The symbol in the parenthesis is the atom to which the hydrogen atom is bonded.

‡ The hydrogen coordinate was not located from three-dimensional difference Fourier syntheses.

Table 2. Observed and calculated structure factors

Columns are: Index, |F\_obs|, |F\_cal|, A\_cal, B\_cal.

\* for unobserved reflections.

Table with columns for Index, |F\_obs|, |F\_cal|, A\_cal, B\_cal, and reflection type. Includes multiple sections for different H and K values (e.g., H=0 K=0, H=2 K=0, H=4 K=0, H=6 K=0, H=8 K=0, H=10 K=0, H=12 K=0, H=14 K=0, H=16 K=0, H=18 K=0, H=20 K=0, H=22 K=0, H=24 K=0, H=26 K=0, H=28 K=0, H=30 K=0). Each section contains rows of numerical data for various reflections.



Table 2 (cont.)

Table with multiple columns of numbers and some mathematical notations like H=, K=, and K=. The table contains numerical data arranged in rows and columns, with some cells containing mathematical expressions such as H=24, K=2 or H=13, K=3.

Table 2 (cont.)

13	67	52	34-	40-	4	78	61	35-	49-	5	180	164	141	83	0	129	120	39	114	0	94	121	72	97								
14	62	90	19	88	5	135	125	96	79	6	94	94	86	39	1	119	100	95-	32	1	102	97	96	15-								
		H=	10	K=	4																											
0	183	178	105	143-		7	134	124	31	120-	8	34*	27	11	25	2	163	165	115-	119-	2	116	137	83	109-							
1	135	136	73-	115-		8	157	153	140	62	9	101	84	83-	13-	3	96	103	64-	81-	3	43*	61	54	29-							
2	204	186	84	166		9	131	115	68-	93	10	122	145	23-	143	5	38*	50	12	49	4	44*	57	57-	8							
3	112	104	94-	45		10	165	167	131-	104-	11	31*	19	10-	17	6	76	62	24	57-	1	35*	23	23	2-							
4	73	81	74-	31		11	72	103	77-	69-	12	81	74	73	9	7	42*	40	38	14-	2	55	47	45	16-							
5	191	174	108-	136-		12	69	59	38	45			H=	-18	K=	4					3	40*	44	42	13							
6	32*	30	1-	30-		13	37*	24	15	19-	3	60	44	22	39	1	137	147	124	78	4	159	134	104	85-							
7	82	89	62	64			H=	14	K=	4	4	120	105	78	70	2	37*	45	35	27	5	70	78	64-	44-							
		H=	-10	K=	4						5	74	51	51-	9	3	88	78	77-	10	6	39*	79	66-	44							
1	106	130	130	13		1	69	74	70	24-	6	93	94	91-	24	4	42*	42	40-	12	7	79	88	87-	12							
2	184	170	131-	108-		2	88	99	59	80	7	31*	38	37-	12	5	41*	51	29-	43-	8	112	121	95-	75							
3	128	116	101	57-		3	100	105	104	9	8	30*	45	44-	11-	6	130	132	57	120-	9	119	143	116	84							
4	45*	75	21-	72-			H=	-14	K=	4	9	119	109	79	74	7	68	62	53-	33-			H=	9	K=	5						
5	62	76	75-	10		1	36*	19	15-	11-			H=	1	K=	5					8	65	79	1	79	0	106	60	28-	54		
6	118	125	70	104		2	74	82	58-	58	0	89	95	19-	93	9	61	79	71-	36	1	42*	57	25	51							
7	93	121	115-	36		3	58	47	39-	26-	1	121	129	123-	36			H=	5	K=	5	2	91	63	55-	31-						
8	78	82	82-	0		4	161	149	10-	148-	2	120	98	54-	81-	0	156	136	104	87			H=	-9	K=	5						
9	166	160	156	37		5	101	93	91	16	3	87	91	87	28	1	116	92	71	59	1	116	102	97-	33-							
10	76	68	8	67		6	101	77	2-	77-	4	106	81	54	60	2	83	90	89-	16	2	151	139	92	104-							
11	57	65	36	55		7	58	67	13-	66	5	70	87	24	84-	3	148	141	128-	59-	3	33*	40	35-	20-							
12	95	74	18-	72-		8	110	104	73-	73	6	90	129	126-	27-	4	66	61	21	57-	4	152	149	109-	102							
13	89	77	64-	43		9	134	124	22-	122-	7	64	50	36	34	5	46*	91	66	63	5	100	82	66	49							
14	82	93	58	73		10	203	192	190	28	8	139	142	142	4-			H=	-5	K=	5	6	33*	34	30-	16						
		H=	12	K=	4						11	92	75	73-	15-			H=	-1	K=	5	1	238	224	224	8-	7	50	54	26-	47	
0	113	108	101-	38-		12	37*	51	29	42	1	58	43	28	32	2	170	166	89	139-	8	63	92	22	89							
1	37*	35	20	28-		13	48	54	50	20	2	37*	34	14	31-	3	205	187	151-	110-			H=	-11	K=	5						
2	126	133	94	94			H=	16	K=	4	3	42*	86	47	72-	4	108	105	104	8-	1	106	112	107	32-							
3	70	58	17	55		0	36*	32	26	19	4	143	134	131-	24-	5	72	60	48	36-	2	63	68	12-	67							
4	79	62	43	44			H=	-16	K=	4	5	132	125	125-	5	6	94	81	8	81-	3	102	79	7-	79							
5	48	37	2-	37-		1	51	53	53-	3-	6	82	45	41	20-	7	60	74	54-	51	4	49	44	7	43							
		H=	-12	K=	4						2	38*	34	25	23	7	38*	27	20	19	8	120	114	78-	83	5	36*	79	76	21-		
1	133	113	98	57-		3	34*	23	16-	16-	8	40*	54	22	49	9	91	119	111	44-	6	63	39	4	39-							
2	222	234	233	8-		4	34*	32	26-	18-			H=	3	K=	5			H=	7	K=	5	7	61	37	27	30					
3	135	134	82	106																												

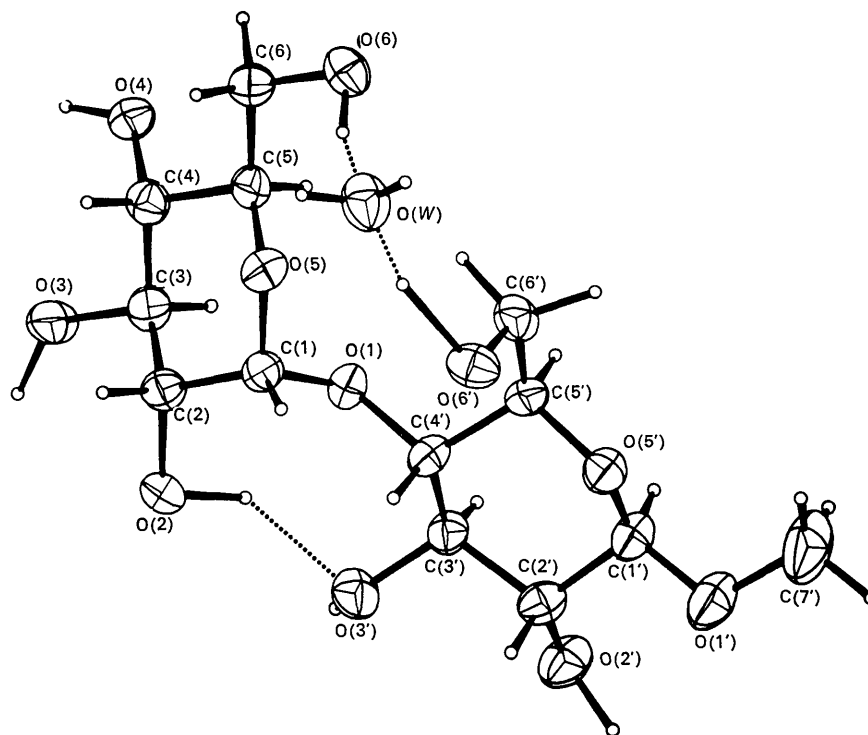


Fig. 1. The structure of one asymmetric unit of methyl  $\beta$ -maltopyranoside monohydrate. Dotted lines are intramolecular hydrogen bonds. The diagram is produced by ORTEP (Johnson, 1965).

O(6')H, on the other side of the molecule. Therefore, the molecule with its associated water forms a relatively rigid four-ring system. Only the hydrogen bond linking O(2) and O(3') was observed in the cyclohexaamylose complex (Hybl *et al.*, 1965). There are two intramolecular hydrogen bonds in the crystal structure of sucrose [O(1')-O(2) and O(5)-O(6')] (Brown & Levy, 1963)

and one in cellobiose [O(5)-O(3')] (Brown, 1966). The packing of the molecules in the crystal appears to be determined mainly by the hydrogen bonds, of which there are nine per asymmetric unit, as illustrated in Fig. 2. Each of the oxygen atoms in the molecule, except the ring oxygen atoms, O(5) and O(5'), and the bridge oxygen atoms, O(1) and O(1'), is associated with

Table 3. *Principal axes of thermal ellipsoids*

The root mean square displacement  $U_i$  corresponds to the  $i$ th principal axis of the ellipsoid, and  $\theta_{ia}$ ,  $\theta_{ib}$ ,  $\theta_{ic}$  are angles between the  $i$ th axis and the crystallographic axes  $a$ ,  $b$ ,  $c$  respectively. The  $B_i$  are equal to the corresponding  $8\pi^2 U_i^2$ .

	$i$	$B_i$	$U_i$	$\theta_{ia}$	$\theta_{ib}$	$\theta_{ic}$
O(1)	1	1.971 Å <sup>2</sup>	0.1580 Å	28.6°	83.0°	144.5°
	2	1.986	0.1586	97.1	151.2	110.9
	3	2.987	0.1945	62.5	117.7	62.7
O(2)	1	1.846	0.1529	70.2	120.8	56.8
	2	3.038	0.1976	159.4	95.6	43.2
	3	4.361	0.2350	84.5	31.4	65.7
O(3)	1	2.067	0.1618	101.0	91.0	16.3
	2	2.516	0.1785	146.0	57.5	75.8
	3	6.248	0.2813	58.3	32.6	97.8
O(4)	1	2.069	0.1619	30.8	120.4	117.0
	2	3.018	0.1955	79.2	64.0	150.2
	3	3.983	0.2246	61.6	42.0	78.4
O(5)	1	1.739	0.1484	65.7	54.5	64.2
	2	2.303	0.1708	153.3	65.9	54.9
	3	3.270	0.2035	100.3	134.7	46.1
O(6)	1	2.245	0.1686	84.8	105.8	35.9
	2	3.184	0.2008	111.1	154.9	91.9
	3	3.846	0.2207	21.8	109.0	125.8
C(1)	1	1.981	0.1584	77.5	14.1	101.5
	2	2.216	0.1675	167.4	77.4	63.3
	3	2.950	0.1933	88.4	83.8	29.5
C(2)	1	1.938	0.1567	56.2	142.6	118.0
	2	2.676	0.1841	73.6	63.0	151.7
	3	2.917	0.1922	38.6	66.2	86.2
C(3)	1	1.826	0.1521	110.4	29.6	61.9
	2	2.490	0.1776	59.9	60.8	149.8
	3	3.189	0.2009	37.7	85.8	79.8
C(4)	1	2.234	0.1682	68.6	21.4	99.9
	2	2.790	0.1880	126.6	76.8	114.3
	3	2.874	0.1908	44.4	106.5	153.6
C(5)	1	1.971	0.1580	38.5	55.7	126.5
	2	2.505	0.1781	123.1	65.5	113.3
	3	3.409	0.2078	107.4	44.5	45.6
C(6)	1	2.181	0.1662	36.1	99.4	82.3
	2	3.003	0.1950	54.4	68.3	155.5
	3	4.261	0.2323	95.2	23.8	66.9
O(1')	1	2.306	0.1709	25.6	90.9	142.8
	2	3.555	0.2122	114.9	104.6	125.6
	3	6.302	0.2825	95.5	14.7	99.5
O(2')	1	1.900	0.1551	39.5	77.2	79.8
	2	3.459	0.2093	50.7	99.8	164.0
	3	5.574	0.2657	93.8	16.2	102.2
O(3')	1	1.779	0.1501	68.1	89.1	49.1
	2	3.232	0.2023	139.4	124.8	51.2
	3	4.732	0.2448	57.7	145.2	115.0
O(5')	1	2.160	0.1654	78.7	83.4	39.2
	2	2.519	0.1786	167.5	93.9	51.0
	3	3.728	0.2173	95.1	7.7	92.7
O(6')	1	2.437	0.1757	54.0	84.3	63.6
	2	2.869	0.1906	82.4	172.3	92.1
	3	4.224	0.2313	37.0	84.8	153.5
C(1')	1	2.118	0.1638	23.9	90.1	141.1
	2	2.426	0.1753	110.6	119.8	123.0
	3	3.762	0.2183	78.5	150.2	71.8



Table 3 (cont.)

	<i>i</i>	<i>B<sub>i</sub></i>	<i>U<sub>i</sub></i>	$\theta_{ia}$	$\theta_{ib}$	$\theta_{ic}$
C(2')	1	2.610	0.1654	28.2	86.7	89.3
	2	2.729	0.1859	67.4	131.6	138.3
	3	3.646	0.2149	105.9	138.3	48.3
C(3')	1	1.642	0.1442	37.2	76.2	82.6
	2	2.282	0.1700	60.6	73.7	163.3
	3	3.555	0.2122	69.3	158.4	104.9
C(4')	1	1.829	0.1522	11.9	97.6	126.0
	2	2.208	0.1672	101.7	119.1	131.5
	3	3.071	0.1972	92.1	149.7	62.3
C(5')	1	1.746	0.1487	32.8	122.8	112.3
	2	2.815	0.1888	76.4	69.2	155.8
	3	2.914	0.1921	60.8	40.4	81.1
C(6')	1	2.049	0.1611	95.5	95.2	22.4
	2	3.005	0.1951	132.2	42.2	71.9
	3	3.769	0.2185	42.7	48.3	102.7
C(7')	1	2.639	0.1838	124.8	97.1	10.5
	2	4.313	0.2337	141.0	103.6	99.3
	3	10.704	0.3682	74.8	164.6	95.0
O( <i>W</i> )	1	2.824	0.1891	82.0	88.6	35.3
	2	3.305	0.2046	135.7	133.5	64.4
	3	5.130	0.2549	46.8	136.4	112.5

two hydrogen bonds, one as donor and one as acceptor, while the water molecule has four hydrogen bonds in distorted tetrahedral configuration, two donor and two acceptor. The water molecules and the oxygens O(6') are joined in a closed four-membered ring of hydrogen bonds around the twofold axes. These closed rings form stacks along the axis which are linked by the hydrogen bonds between the water molecules and the other primary alcoholic oxygen atoms, O(6). The other hydrogen bonds form helical chains extending in the *b*-axis direction with 3 and 4 hydrogen bonds per repeat unit of the helix. The 4-unit helices link the atoms O(2) and O(3') and their symmetry relations around the two-

fold screw axes. These helices are right-handed with the donor-acceptor sequence O(2)→O(3')→O(2)→O(3'). The hydroxyls at O(2'), O(3), O(4) and their translational relations form the 3-unit helices. These helices are left-handed with the sequence O(2')→O(3)→O(4). Thus there is a tendency for the polarity resulting from these helices of polar bonds to be balanced in the polar direction of the crystal. In this structure, however, there are twice as many 3-unit left-handed helices as 4-unit right-handed ones. Similar helices of hydrogen bonds have been observed in other carbohydrate structures. In methyl-1-thio- $\beta$ -D-xylopyranoside, which is triclinic *P*1, there are two symmetry unrelated 3-unit helices with opposite senses (Mathieson & Poppleton, 1966). In methyl- $\alpha$ -glucose (Berman & Kim, 1967), there are left and right-handed 3-unit helices by reason of the non-polar space group, *P*2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>. Similarly, in  $\alpha$ -methyl-D-galactoside-6-bromohydrin (Robertson & Sheldrick, 1965) the 6-unit helices which spiral around the screw axes are paired in opposite senses by the space group symmetry. All the available hydrogen atoms of the hydroxyl groups are used in hydrogen bond formation. The hydrogen atom H(O6') was observed closer to O(*W*) than to O(6') by 1.29 versus 1.54 Å. While there are no indications of abnormally large errors associated with that particular hydrogen peak on the difference maps, this is a result that requires confirmation by an independent experiment. The hydrogen bond distances and angles are shown in Table 5. The non-bonded distances which are less than 3.3 Å are also listed in Table 5.

The bond lengths and bond angles with their standard deviations are shown in Table 6. The C-C bond lengths range from 1.510 to 1.535 Å and none differ

Table 4. Conformation angles\*

Within the pyranose rings

C(1) → C(2)	+56.2°	C(1') → C(2')	+55.7°
C(2) → C(3)	-58.4	C(2') → C(3')	-50.0
C(3) → C(4)	+60.5	C(3') → C(4')	+52.0
C(4) → C(5)	-60.1	C(4') → C(5')	-58.3
C(5) → O(5)	+58.3	C(5') → O(5')	+65.1
O(5) → C(1)	-56.2	O(5') → C(1')	-64.9

Outside the pyranose rings

Bond	Reference atoms	Conformation angle
C(5) → C(6)	O(5) C(5) C(6) O(6)	+60.4°
C(5') → C(6')	O(5) C(5) C(6') O(6')	-67.9
C(1') → O(1')	O(5') C(1') O(1') C(7')	-69.2
O(1) → C(1)	C(4') O(1) C(1) C(2)	-128.2
	C(4') O(1) C(1) O(5)	+110.0
O(1) → C(4')	C(1) O(1) C(4') C(3)	+129.2
	C(1) O(1) C(4') C(5)	-108.9

\* The conformation angle of a directed bond C(2) → C(3) is defined as the angle, measured counter-clockwise, that the projection of the bond C(1) → C(2) makes with respect to the projection of the bond C(3) → C(4). The angle is positive if it is measured clockwise (Klyne & Prelog, 1960).

Table 5. *Hydrogen bond distances and angles*

<i>i</i>	<i>j</i>	<i>k</i>	<i>D</i> ( <i>ij</i> )	<i>D</i> ( <i>jk</i> )	Angle <i>ijk</i>
C(2)	O(2)	O(3')		2.825 Å	118.2°
C(2)	O(2)	O(3') ( <i>a</i> )		2.694	140.9
C(3)	O(3)	O(4) ( <i>b</i> )		2.762	135.0
C(3)	O(3)	O(2') ( <i>a</i> )		2.877	131.1
C(4)	O(4)	O(3) ( <i>b</i> )		2.762	94.4
C(4)	O(4)	O(2') ( <i>c</i> )		2.997	148.0
C(6)	O(6)	O( <i>W</i> )		2.859	113.3
C(6)	O(6)	O( <i>W</i> )( <i>d</i> )		2.769	121.4
C(2')	O(2')	O(3) ( <i>e</i> )		2.877	150.9
C(2')	O(2')	O(4) ( <i>f</i> )		2.997	115.5
C(3')	O(3')	O(2)		2.825	117.8
C(3')	O(3')	O(2) ( <i>e</i> )		2.694	104.1
C(6')	O(6')	O( <i>W</i> )		2.802	103.5
C(6')	O(6')	O( <i>W</i> )( <i>g</i> )		2.803	104.0
O(6)	O( <i>W</i> )	O(6) ( <i>h</i> )	2.859 Å	2.769	118.7
O(6')	O( <i>W</i> )	O(6') ( <i>g</i> )	2.802	2.803	79.0
O(6)	O( <i>W</i> )	O(6') ( <i>e</i> )	2.859	2.802	96.9
O(6)	O( <i>W</i> )	O(6') ( <i>g</i> )	2.859	2.803	108.1
O(6)( <i>h</i> )	O( <i>W</i> )	O(6') ( <i>e</i> )	2.769	2.802	114.7
O(6)( <i>h</i> )	O( <i>W</i> )	O(6') ( <i>g</i> )	2.769	2.803	127.9
O( <i>W</i> )	O(6)	O( <i>W</i> )( <i>d</i> )	2.859	2.769	118.7
O( <i>W</i> )	O(6')	O( <i>W</i> )( <i>g</i> )	2.802	2.803	97.7

Intermolecular non-bonded distances less than 3.3 Å.

<i>i</i>	<i>j</i>	<i>D</i> ( <i>ij</i> )
O(3)	O(3)( <i>b</i> )	3.300 Å
O(3)	C(4)( <i>b</i> )	3.208
O(5)	O( <i>W</i> )	3.257

Table 5 (*cont.*)

Symmetry Code			
	<i>x</i>	<i>y</i>	<i>z</i>
<i>a</i>	$\frac{1}{2}-x$	$\frac{1}{2}+y$	$-z$
<i>b</i>	$1-x$	<i>y</i>	$-z$
<i>c</i>	$\frac{1}{2}+x$	$-\frac{1}{2}+y$	<i>z</i>
<i>d</i>	$-x$	$-1+y$	<i>z</i>
<i>e</i>	$\frac{1}{2}-x$	$-\frac{1}{2}+y$	$-z$
<i>f</i>	$-\frac{1}{2}+x$	$\frac{1}{2}+y$	<i>z</i>
<i>g</i>	$1-x$	<i>y</i>	$1-z$
<i>h</i>	<i>x</i>	$1+y$	<i>z</i>

significantly from the mean value of 1.520 Å. The C–O bond lengths, excluding the C(1')–O(1'), range from 1.408 to 1.440 Å with the mean value of 1.427 Å. The bond length of C(1')–O(1') is 1.375 Å, which is shorter than the mean value by  $7\sigma$ . The comparative shortening of a C(1)–O(1)H link has been observed in five other structure determinations of pyranose sugars at significant levels varying between ( $\Delta=2\sigma$ ) and ( $\Delta=7\sigma$ ), but this is the first such observation in a glucoside derivative (*cf.* Kim & Jeffrey, 1967). In contrast, the corresponding  $\alpha$ -glycosidic link, C(1)–O(1), is 1.416 Å, which is not significantly different from the mean value. Associated with this normal C–O bond length, there is an apparent inequality of the ring C–O bonds. That adjacent to the anomeric C(1) is shorter by 0.032 Å,

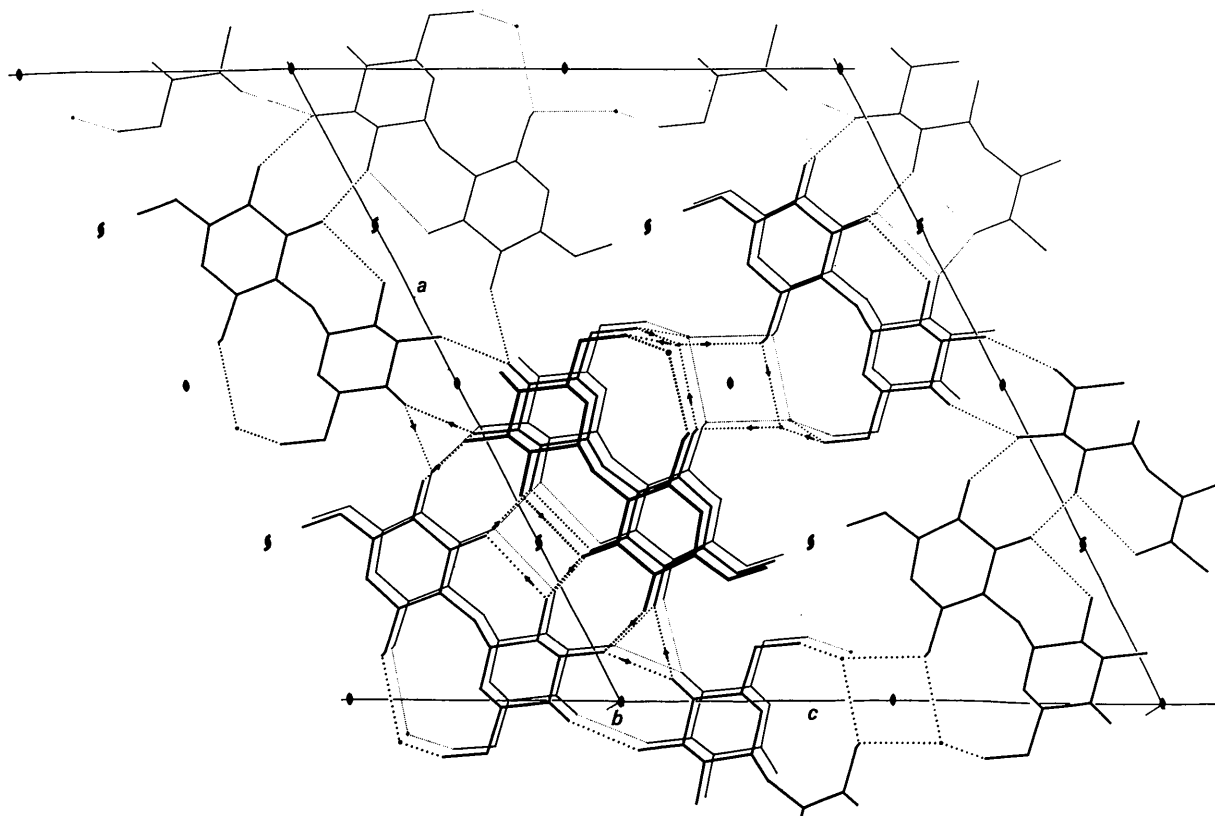


Fig. 2. The molecular packing and hydrogen bonding in methyl  $\beta$ -maltopyranoside monohydrate. The dotted lines are hydrogen bonds. The arrows indicate the donor-acceptor direction.

which corresponds to  $3.5\sigma$  and is therefore probably significant. The acceptance of this as a characteristic feature associated with an 'unshortened' glucosidic link is strongly supported by a similar result observed in

Table 6. Bond lengths and bond angles (with estimated standard deviations in parentheses referred to the last decimal positions of respective values)

C(1)–C(2)	1.514 (8) Å	O(5)–C(1)–O(1)	111.5 (4)°
C(2)–C(3)	1.516 (8)	C(2)–C(1)–O(1)	107.8 (5)
C(3)–C(4)	1.531 (8)	C(2)–C(1)–O(5)	110.9 (5)
C(4)–C(5)	1.533 (8)	C(1)–C(2)–O(2)	110.2 (5)
C(5)–C(6)	1.526 (9)	C(3)–C(2)–O(2)	112.4 (5)
		C(1)–C(2)–C(3)	111.1 (5)
C(1)–O(1)	1.416 (7)	C(2)–C(3)–O(3)	110.4 (5)
C(1)–O(5)	1.408 (7)	C(4)–C(3)–O(3)	108.6 (5)
C(2)–O(2)	1.428 (7)	C(2)–C(3)–C(4)	106.1 (5)
C(3)–O(3)	1.422 (8)	C(3)–C(4)–O(4)	111.1 (5)
C(4)–O(4)	1.435 (7)	C(5)–C(4)–O(4)	109.4 (5)
C(5)–O(5)	1.440 (7)	C(3)–C(4)–C(5)	109.1 (5)
C(6)–O(6)	1.428 (8)	C(4)–C(5)–O(5)	108.8 (5)
		C(6)–C(5)–O(5)	106.4 (5)
C(1')–C(2')	1.510 (9)	C(4)–C(5)–C(6)	111.7 (5)
C(2')–C(3')	1.535 (8)	C(5)–C(6)–O(6)	111.4 (5)
C(3')–C(4')	1.513 (8)		
C(4')–C(5')	1.512 (8)	O(5')–C(1')–O(1')	107.1 (5)
C(5')–C(6')	1.513 (9)	C(2')–C(1')–O(1')	108.9 (5)
		C(2')–C(1')–O(5')	110.3 (5)
C(1')–O(1')	1.375 (8)	C(1')–C(2')–O(2')	110.9 (5)
C(1')–O(5')	1.427 (7)	C(3')–C(2')–O(2')	107.7 (5)
C(2')–O(2')	1.419 (8)	C(1')–C(2')–C(3')	109.8 (5)
C(3')–O(3')	1.429 (7)	C(2')–C(3')–O(3')	111.1 (5)
C(4')–O(1)	1.438 (7)	C(4')–C(3')–O(3')	107.4 (5)
C(5')–O(5')	1.430 (7)	C(2')–C(3')–C(4')	110.7 (5)
C(6')–O(6')	1.437 (8)	C(3')–C(4')–O(1)	107.9 (4)
C(7')–O(1')	1.425 (11)	C(5')–C(4')–O(1)	111.1 (5)
		C(3')–C(4')–C(5')	111.0 (5)
		C(4')–C(5')–O(5')	108.2 (5)
		C(6')–C(5')–O(5')	108.4 (5)
		C(4')–C(5')–C(6')	115.3 (5)
		C(5')–C(6')–O(6')	110.7 (5)
		C(1)–O(1)–C(4')	117.6 (4)
		C(1)–O(5)–C(5)	114.7 (4)
		C(1')–O(1')–C(7')	113.2 (6)
		C(1')–O(5')–C(5')	111.5 (4)

the  $\alpha$ -glucopyranose residue of sucrose at a higher significance level ( $10\sigma$ ) by Brown & Levy (1963). The C–O bond lengths in the three disaccharides which have been studied are summarized in Table 7. The results of this work and of that on sucrose are consistent with the data on the monosaccharides (Kim & Jeffrey, 1967), if the following 'rules' are adopted:

I. An axial glycosidic bond is short only when the hydrogen atom on O(1) is unsubstituted, as suggested by Robertson & Sheldrick (1965).

II. An equatorial glycosidic C(1)–O(1) bond is short irrespective of whether the hydrogen atom on O(1) is substituted or not.

III. When there is a shortening of the C(1)–O(1) bond length, no significant differences have been observed in the ring C–O bond lengths.

IV. If the C(1)–O(1) bond is not significantly short, the two ring C–O bond lengths are possibly different, with that adjacent to the glycosidic link the shorter.

These bonds form the hemiacetal group of the pyranose ring, the properties of which give rise to much of the variety in carbohydrate chemistry in aqueous solution. It is well known to be very sensitive to intra- and inter-molecular environments, but no theoretical treatment has yet been suggested which could provide a basis for comparison with these observations.

Valence angles lie within the range commonly found in pyranose sugars (*cf.* Jeffrey & Rosenstein, 1964). The internal angles of the carbon atoms in the rings range from  $106.1$  to  $111.1^\circ$ , with the mean value of  $109.4^\circ$ , and those outside the ring range from  $107.1$  to  $115.2^\circ$  with the mean value of  $110.0^\circ$ . The valence angles of the ring oxygen atoms are  $114.7$  and  $111.5^\circ$ . The angle at the  $\beta$ -glycosidic oxygen is  $113.2^\circ$  and that joining the two glucopyranose units is  $117.6^\circ$ , which compares with  $116.7^\circ$  in cellobiose (Brown, 1966),  $114.4^\circ$  in sucrose (Brown & Levy, 1963) and  $119.1^\circ$  in cyclohexaamylose-potassium iodide (Hybl *et al.*, 1965). The configuration of the molecule, the intra- and

Table 7. Comparison of C–O bond lengths in disaccharides

	Configuration of C(1)–O(1) bond	Bond length of C(1)–O(1)	Shortening of C(1)–O(1) bond (from mean)	Bond length of ring C–O		Difference between two ring C–O bond lengths
				C(1)–O(5)	C(5)–O(5)	
Methyl $\beta$ -maltoside monohydrate (Chu & Jeffrey, this work)	axial*	1.416	$1.5\sigma$	1.408	1.440	$3.5\sigma$
	equatorial†	1.375	$7\sigma$	1.427	1.430	none
Cellobiose (Brown, 1966)	equatorial*	1.373	$7\sigma$	1.458	1.406	$6\sigma$
	equatorial‡	1.389	$5\sigma$	1.453	1.423	$3.5\sigma$
Cellobiose (Jacobson <i>et al.</i> , 1961)	equatorial*	1.38	$2.5\sigma$	1.45	1.38	$2.5\sigma$
		(1.43)§	(none)	(1.46)	(1.43)	( $1.5\sigma$ )
	equatorial‡	1.40	$1.5\sigma$	1.35	1.47	$4\sigma$
		(1.41)	(none)	(1.38)	(1.43)	( $2.5\sigma$ )
Sucrose residue ( $\alpha$ -glucose) (Brown & Levy, 1963)	axial*	1.420	none	1.408	1.436	$10\sigma$

\* C–O–sugar.

† C–OCH<sub>3</sub>.

‡ C–OH.

§ Values in parentheses are results from anisotropic refinement of these data by Sundaralingam (1965).

$\sigma$  = Estimated standard deviations as quoted by authors.

intermolecular distances and bond angles were calculated with IBM 1620 programs by Chu & Shiono (1963).

The thermal ellipsoid parameters given in Table 3 and the illustration in Fig. 1 (Johnson, 1965) show that the molecule as a whole has no marked thermal anisotropy. As in the structure of cellobiose (Brown, 1966), all the oxygen atoms appear to have higher vibration amplitudes perpendicular to their C-O bonds than along them. The methyl group has a high thermal motion consistent with its van der Waals environment around the twofold axes (see Fig. 2).

This research has been supported by the U.S. Public Health Service, National Institutes of Health, through Grant GM 11293. We wish to thank Dr R. Bentley for providing the crystals and discussing the chemistry of maltose, Dr P. W. R. Corfield for making the convolution computation, Dr R. Shiono for his help in using his computer programs and Dr R. Rosenstein for suggestions in preparing this manuscript.

#### References

- BENTLEY, R. (1959). *J. Amer. Chem. Soc.* **81**, 1952.  
 BERMAN, H. & KIM, S. H. (1967). To be published.  
 BEURSKENS, P. T. (1963). *Sign Correlation by the Sayre Equation*. Technical Report, The Crystallography Lab., Univ. of Pittsburgh.  
 BROWN, C. J. (1966). *J. Chem. Soc. (A)* p.927.  
 BROWN, G. M. & LEVY, H. A. (1963). *Science*, **141**, 921; and private communication.  
 BUSING, W. R., MARTIN, K. O. & LEVY, H. A. (1962). *Fortran Crystallographic Least Squares Program*. ORNL-TM-305, Oak Ridge National Laboratory, Tennessee.  
 CHU, S. C. & SHIONO, R. (1963). *Technical Reports* 43 and 45, Crystallography Lab. Univ. of Pittsburgh.

- CORFIELD, P. W. R. (1965). *Solution of the Patterson Function by Superposition Methods*. Technical Report, Crystallography Lab. Univ. of Pittsburgh.  
 CRUICKSHANK, D. W. J. (1961). In *Computing Methods and the Phase Problem in X-ray Crystal Analysis*. New York: Pergamon Press.  
 HAMILTON, W. C., ROLLETT, J. S. & SPARKS, R. A. (1965). *Acta Cryst.* **18**, 129.  
 HAUPTMAN, H. & KARLE, J. (1953). *Solution of the Phase Problem. I. The Centrosymmetric Crystal*. A.C.A. Monograph no. 3. Ann Arbor, Mich.: Edward Bros.  
 HAWORTH, W. N., LONG, C. W. & PLANT, J. H. G. (1927). *J. Chem. Soc.* p.2809.  
 HUGHES, E. W. (1941). *J. Amer. Chem. Soc.* **63**, 1737.  
 HYBL, A., RUNDLE, R. E. & WILLIAMS, D. E. (1965). *J. Amer. Chem. Soc.* **87**, 2779.  
 JACOBSON, R. A., WUNDERLICH, J. A. & LIPSCOMB, W. N. (1961). *Acta Cryst.* **14**, 598.  
 JEFFREY, G. A. & ROSENSTEIN, R. D. (1964). *Advanc. Carbohydrate Chem.* **19**, 7.  
 JOHNSON, C. K. (1965). *A Fortran Thermal-Ellipsoid Plot Program for Crystal Structure Illustrations*. ORNL 3794. Oak Ridge National Laboratory, Tennessee.  
 KARLE, I. L., HAUPTMAN, H., KARLE, J. & WING, A. B. (1958). *Acta Cryst.* **11**, 257.  
 KIM, S. H. & JEFFREY, G. A. (1967). *Acta Cryst.* **22**, 537.  
 KLYNE, W. & PRELOG, V. (1960). *Experientia*, **16**, 521.  
 MATHIESON, A. MCL. & POPPLETON, B. J. (1966). *Acta Cryst.* **21**, 72.  
 ROBERTSON, J. H. & SHELDRIK, B. (1965). *Acta Cryst.* **19**, 820.  
 SAYRE, D. (1952). *Acta Cryst.* **5**, 60.  
 SHIONO, R. (1966a). *Data Reduction and Scaling Fortran Program*. The Crystallography Lab., Univ. of Pittsburgh.  
 SHIONO, R. (1966b). Oak Ridge Least-Squares Program Modified for the Crystallography Lab. of the Univ. of Pittsburgh.  
 SUNDARALINGAM, M. (1965). Private communication.

*Acta Cryst.* (1967). **23**, 1049

### Crystal Structure of Ethyl-1-thio- $\alpha$ -D-glucufuranoside

BY R. PARTHASARATHY AND RAYMOND E. DAVIS\*

Center for Crystallographic Research, Roswell Park Division of Health Research, Inc., 666 Elm Street, Buffalo, New York 14203, U.S.A.

(Received 20 February 1967)

The crystal structure of ethyl-1-thio- $\alpha$ -D-glucufuranoside (C<sub>8</sub>H<sub>16</sub>O<sub>5</sub>S) has been determined by three-dimensional Patterson and Fourier syntheses. The structure was refined by block-diagonal least squares. The final *R* value for the structure with the correct absolute configuration was 8.9% for the 1030 observed reflections. The absolute configuration of the molecule was determined from the anomalous scattering of Cu *K* $\alpha$  radiation by the sulfur atom. The geometry of the molecules is, in general, in accord with previous studies on monosaccharides. The conformation of the furanose ring seems to be slightly different from that observed in other compounds. The stacking of the molecules and the hydrogen bonding scheme are illustrated.

#### Introduction

The furanose ring occurs in a variety of important biological molecules, particularly in the nucleic acids

and other carbohydrate derivatives. Information on the conformations of the furanose moieties is of considerable importance in nucleic acid model building. The present study on ethyl-1-thio- $\alpha$ -D-glucufuranoside was undertaken in order to supply additional precise information about the stereochemistry of furanoid rings.

\* Present address: University of Texas, Chemistry Department, Austin, Texas, U.S.A.